

THIS PAGE BLANK (USPTO)

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: Apr 13, 2000, 03:22:17 ; Search time 528.89 seconds
(without alignments)
-6028.103 Million cell updates/sec

Title: US-09-459-774-1

Perfect score: 1050
Sequence: 1 atgacgcgaaagcgcgcg.....agatgtacacgtgcgaagtga 1050

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Search: 821193 seqs, -1518192014 residues

Total number of hits satisfying chosen parameters: 1642386

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_dal: *
2: gb_ba2: *
3: gb_om: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
7: gb_p11: *
8: gb_p12: *
9: gb_p12: *
10: gb_p12: *
11: gb_p13: *
12: gb_ro: *
13: gb_sts: *
14: gb_sy: *
15: gb_un: *
16: gb_v1: *
17: em_fun: *
18: em_hum1: *
19: em_hum2: *
20: em_in: *
21: em_om: *
22: em_or: *
23: em_ov: *
24: em_pat: *
25: em_ph: *
26: em_p1: *
27: em_ro: *
28: em_sts: *
29: em_sy: *
30: em_un: *
31: em_v1: *
32: gb_htg1: *
33: gb_htg2: *
34: gb_in1: *
35: gb_in2: *
36: em_ba1: *
37: em_ba2: *
38: em_hum3: *
39: em_hum4: *
40: gb_p14: *
41: gb_htg3: *
42: gb_htg4: *
43: gb_htg5: *
44: gb_htg6: *

45: gb_htg7: *
46: em_htg1: *
47: em_htg2: *
48: em_htg3: *
49: em_hum5: *
50: gb_p13: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045.2	99.5	1442	9 D83175	D83175 Homo sapien
2	1038.8	98.9	1469	11 HS053476	U53476 Human prolo
3	926.8	88.3	1050	12 MUSMNTVIA	M89801 Mouse Wnt-7
4	678.8	64.6	1449	12 MUSMNTVIB	M89802 Mouse Wnt-7
5	675.6	64.3	1948	4 PM080581	U80581 Pleurodeles
6	586	55.8	1199	4 AF026894	AF026894 Xenopus 1
7	482.2	45.9	245767	42 AC011607	AC011607 Homo sapi
8	479.6	45.7	1661	35 AF061975	AF061975 Branchios
9	297.4	28.3	1427	4 CHKMAP	D31900 Chicken mRN
10	292.6	27.9	1292	4 AF182403	AF182403 Gallus ga
11	289.4	27.6	1213	12 AF188608	AF188608 Rattus no
12	283	27.0	1101	12 MUSMNTIV	M89797 Mouse Wnt-4
13	283	27.0	1252	34 DMDMNT2MR	X64735 D.melanogas
14	283	27.0	1500	12 AF070988	AF070988 Mus muscu
15	276.8	26.4	3000	12 MUSINT4	M32502 Mouse proto
16	275	26.2	245767	42 AC011607	AC011607 Homo sapi
17	272.8	26.0	4114	9 HDMNT5A	L20861 Homo sapien
18	261.2	24.9	2385	9 HSNMT13	Z71621 H.sapiens W
19	254.6	24.2	2664	4 AMMNT5B	Z14048 A.mexicanum
20	252.2	24.0	369	4 PLEMT7A	M91295 Plethodon j
21	248.8	23.7	1523	12 MUSMNTVB	M89799 Mouse Wnt-5
22	248.8	23.7	1690	12 MUSMNTVA	M89798 Mouse Wnt-5
23	248.8	23.7	1980	12 AP188333	AF188333 Rattus no
24	245.2	23.4	3056	35 AF061973	AF061973 Branchios
25	244	23.2	1509	4 DR051266	U51266 Danio rerio
26	243.2	23.2	369	4 GOOMNT7A	M91261 Chen caerul
27	241.6	23.0	369	4 TKYMT7A	M91285 Meleagris g
28	241	23.0	1059	4 DR05141	U25141 Danio rerio
29	240.2	22.9	2814	12 MMAMNT3A	X56842 Mouse mRNA
30	236	22.5	372	4 XELMNT7A	L07533 Xenopus lae
31	235.6	22.4	2301	9 HSIIRP	X07876 Human mRNA
32	235	22.4	1543	4 AB006014	AB006014 Gallus ga
33	234.8	22.3	2076	35 SPUS8982	U56982 Strongyloce
34	234.6	22.3	1778	4 DR051267	U51267 Danio rerio
35	233.4	22.2	2230	12 MUSINT1M	M11943 Mouse int-1
36	233.2	22.2	1272	5 AR018070	AR018070 Sequence
37	226	21.5	3574	4 AMMNT5A	Z14047 A.mexicanum
38	224.6	21.4	1151	4 AB024080	AB024080 Gallus ga
39	223.2	21.3	1160	4 PM080582	U80582 Pleurodeles
40	219.6	20.9	1730	4 DR051268	U51268 Danio rerio
41	219.4	20.9	1188	4 XLMKNT5C	X73510 X.laevis xv
42	218.6	20.8	369	4 EPTWNT7I	M91269 Eptatretus
43	210.6	20.1	369	4 AOPMNT7A	M91256 Alopiax vul
44	210.4	20.0	372	4 XELMNT7B	L07534 Xenopus lae
45	210	20.0	2372	35 AF061974	AF061974 Branchios

ALIGNMENTS

RESULT 1
D83175 LOCUS D83175 1442 bp mRNA
DEFINITION Homo sapiens WNT7A mRNA, complete cds.
ACCESSION D83175
VERSION D83175.1 GI:5509900
KEYWORDS WNT7A.

PRI

16-JUL-1999

SOURCE Homo sapiens tissue_l1b:placenta cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
AUTHORS Ikegawa,S., Kumano,Y., Okui,K., Fujiwara,T., Takahashi,E. and Nakamura,T.
TITLE Isolation, characterization and chromosomal assignment of the human WNT7A gene
JOURNAL Cytogenet. Cell Genet. 74 (1-2), 149-152 (1996)
MEDLINE 97049094
REFERENCE 2 (bases 1 to 1442)
AUTHORS Nakamura,Y.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1996) to the DDBJ/EMBL/GenBank databases. Yusuke Nakamura, Institute of Medical Science, The University of Tokyo, Laboratory of Molecular Medicine: 4-6-1 Shirokanebashi, Minato-ku, Tokyo 108, Japan (E-mail:sikegawa@ims.u-tokyo.ac.jp, Tel:+81-3-5449-5372, Fax:+81-3-5449-5433)
FEATURES
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BASE COUNT 319 a 432 c 420 g 271 t
ORIGIN
Query Match 99.5%; Score 1045.2; DB 9; Length 1442;
Best Local Similarity 99.7%; Pred. No. 2.3e-188;
Matches 1047; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Oy 421 taccacccggagcggggctggaagtgggtgctgctcctgcacacacgctaagcctc 480
Db 451 TACCAACGGGACGAGGGCTGGAAATGGGGTGGCTCTGCGGCATCTCCGTACGGCATC 510
Oy 481 gcttcgccaaagctcttctgtgatcccggaagatcaagcaaatgcccgaactcatg 540
Db 511 GCGTTGCGCAAGGCTTGTGTGATGCCCGGAGATCAAGCAAGATGCCGAGCTTCATG 570
Oy 541 aacttgcaacaacagcagcagcagcgaagaatccttgtaggaagaatgaagctggaatg 600
Db 571 AACTTGCAACAACAGAGCGAGCGCAAGATCTTGAGAGGAACATGAAGCTGGAATGT 630
Oy 601 aagtgccacggcgtgtgaagctgtgtgaccccaagacggtgtgacgaactccacag 660
Db 631 AAGTGCCACGGCGGTGAGGCTGTGACACCAAGAGCTGTGGACCACTGCGCAG 690
Oy 661 ttccggagctgggtctacgtgtcacaagacaaagatacgaagccgtctcagtgagcct 720
Db 691 TTTCGGGAGCTGGGCTACGTGCTCAAGGACAAAGTACACGAGCGCGTTCACTGAGCCT 750
Oy 721 gtgcgtgcagcgcgaacaagcggccacacttccctgaagatcaagaagcactgtgtac 780
Db 751 GTGCGTGACACCGCAACAGCGGCCACCTCTGAAAGATCAAGAAAGCACTGCTCTAC 810
Oy 781 cgaagcccatggaacagagcctgtgtacatgagaagatgcccaactactgtagagag 840
Db 811 CGCAAGCCCATGACACGAGACTGTGTACTCATGAGAAATGCCCACTACTGCGAGAG 870
Oy 841 gaccgggtgacccgacgtgtgtgacccagggccgcctgcgaacaagaagcctccacag 900
Db 871 GACCGGGTACCGGACAGTGTGGCACCCAGGCGCGCTGCACAAAGAGCGCTCCACAG 930
Oy 901 gccagcggctgtgacctcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
Db 931 GCCAGCGGCTGTGACCTCATGTGCTGTGGGGGTGTGTGTGTGTGTGTGTGTGTGTGT 990
Oy 961 gt 1020
Db 991 GTGTGGCATGCTCACTGTAATTCATTCATGATGTGTGTGTGTGTGTGTGTGTGTGTGT 1050
Oy 1021 gaggcagcagagatgtacacgtgcaagtga 1050
Db 1051 GAGCGCAGGAGATGTACAGTGCAGATGA 1080
RESULT 2
HSU53476
LOCUS HSU53476 1469 bp mRNA PRI 19-MAY-1997
DEFINITION Human proto-oncogene Wnt7a mRNA, complete cds.
ACCESSION U53476
VERSION U53476.1 GI:2105099
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1469)
AUTHORS Bul,T.D., Lejeune,S., Curtis,A.R., Strachan,T., Lindsay,S. and Harris,A.L.
TITLE Isolation of a full-length human WNT7A gene implicated in limb development and cell transformation, and mapping to chromosome 3p25
JOURNAL Gene 189 (1), 25-29 (1997)
MEDLINE 97305141
REFERENCE 2 (bases 1 to 1469)
AUTHORS Bul,T.D., Lejeune,S. and Harris,A.L.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1996) T.D. Bul, Imperial Cancer Research Fund, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK
FEATURES
Location/Qualifiers

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1. 1469
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/db_xref="taxon:9606"
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/dev_stage="17-week embryo"
/clone="ICRFp507A0938"
/vector, generated by oligo dt priming (from ICRF library
number 507), cloning sites: NotI and SalI"
25. 1074
/gene="Wnt7a"
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/function="signal patterning"
/note="proto-oncogene; signal transducer"
/codon_start=1
/product="Wnt7a protein"
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/db_xref="GI:2105100"
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GFAKVFIDAREIKONARTLMLHNNEGRKILBNMLCEKCHGVSSCTTKTCWTL
PQRELDYVLKDKYNEAVHVEPVASNNKPTFLIKPLSYRPMOTDLVLEKSPN
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KCNCSERTEMYTCK"

BASE COUNT      347 a      435 c      416 g      271 t
ORIGIN

Query Match      98.9%; Score 1038.8; DB 11; Length 1469;
Best Local Similarity 99.3%; Pred. No. 3,7e-187;
Matches 1043; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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DB 25 ATGAACGGAAAGCGCTGCTGCTGGGCCACCTCTTCTCAAGCTGGCGATGGTCTGC 84
    |||||||

QY 61 ctccgagatcggtgcttctcctcaatgtagctctggcgcaagatcatctgtacaag 120
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DB 85 CTCGGAGTCGGTGGCTTCTCTCACTGTAAGTCTGGGGGCAACATCATCTGTACACAG 144
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QY 121 atcccaagccttgctcccaagaacgagcgatctgcagagccgagcccgacatc 180
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QY 241 cgtctgaactctctgctctggagagagcgccctcttcggaagaagatcaaatgg 300
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DB 265 CGCTGGAATCTGCTGCACTGGAGAGGCGACAGCTTCTGGGAAAGAGCTCAAAATGGGG 324
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DB 325 AGCCGGAGAGCGTCTTCACTACCTACCATCATCTGCCGGGGGTGGCCACGCCATCACA 384
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QY 661 ttctggagagctggagctcgtgtgtcacaagaagatgacagagcgcttcaagtgaagc 720
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DB 685 TTCTGGAGAGCTGGGCTGTACGCTCAAGAGACAGTACACAGAGGCGCTTCAAGTGAAGCCT 744
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QY 721 gttgctccagcgccgaacaagcgccacgtctctgtaagatcaagaagcactgtctac 780
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DB 805 CGCAAGCCCATGAGACAGGAGACTGTGTACATCGAAGAGTCCGCCCACTACTGCGAGAG 864
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QY 841 gaccggtgacagcgcaagtgtggcaccagagcgccgctgtcaacaagaagcgctccag 900
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RESULT 3
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1050)
Gavin,B.J., McMahon,J.A. and McMahon,A.P.
Expression of multiple novel Wnt-1/Int-1-related genes during fetal
and adult mouse development
Genes Dev. 4, 2319-2332 (1990)
JOURNAL
MEDLINE
91122634
REFERENCE
2 (sites)
Gavin,B.J. and McMahon,A.P.
Differential regulation of the Wnt gene family during pregnancy and
lactation suggests a role in postnatal development of the mammary
gland
Mol. Cell. Biol. 12, 2418-2423 (1992)
JOURNAL
MEDLINE
92236617
FEATURES
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1. 1050
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BASE COUNT 234 a 296 c 324 g 196 t
ORIGIN

Query Match 88.3%; Score 926.8; DB 12; Length 1050;
Best Local Similarity 92.7%; Pred. No. 5.4e-166;
Matches 973; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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OY 61 ctccggatcgctgctctcctcaagtgtgactctggcgcaagatcatctgtacaag 120
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DB 661 TTCCAGAGACTAGCTACTCTCAAGGACAATACAAAGAGCGCTCCACGCTGAGCTT 720
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DB 721 GTGCTGCGAGTCGAAAGAGCGCCACCTTCTGAATATCAAGAGCGCCCTGTCTTAC 780
OY 781 cgaagacccatgagacagagacgtgtgtatcatcagaaagtcgcccacactcgtcgagag 840
DB 781 CGCAAGCCCATGAGACACTGACTGTGTATATCGAGTTTCAACCAATATACGTGAAGAG 840
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DB 841 gaaccgtagacggaggtgtgggcaaccagggcgcgctgtcaacaagaagcgtctccccc 900
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OY 901 gccacggcctgtgacctgactgtgctgtggcggtgtgctacaaacaccacagtagcggcgc 960
DB 901 GCCAGTGGCTGTGACCTATATGTCTGTGGCCGTGCTTCAACACACACAGCTACGCCGG 960
OY 961 gtagtgcaagctgcaactgtgaattcccaactgtgctgtctatgtcgaagtgcacaagctgca 1020
DB 961 GTGTGCGAGTGCACACTGCAAAATTCACACTGCTGTGCTACGTCAAGTGTAAACAGTGCAGC 1020
OY 1021 gagcgacgagagatgatacagctgcaagtga 1050
DB 1021 GAGCGACGAGAGATGTATACGTGCAAGTGA 1050
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RESULT 4

MUSMNTVIIB 1449 bp mRNA ROD 27-APR-1993
LOCUS Mouse Wnt-7b mRNA, complete cds.
DEFINITION M89802
ACCESSION M89802.1 GI:202411
VERSION Wnt-1 related protein: Wnt-7b; Int-1 related protein.
KEYWORDS Mus musculus (strain C57/BL6) (library: lambda cDNA) 8.5 day embryo
SOURCE cDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 1449)
Gavin,B.J., McMahon,J.A. and McMahon,A.P.
Expression of multiple novel Wnt-1/Int-1-related genes during fetal
and adult mouse development
Genes Dev. 4, 2319-2332 (1990)

JOURNAL

9112634
MEDLINE
AUTHORS Gavin,B.J. and McMahon,A.P.
TITLE Differential regulation of the Wnt gene family during pregnancy and
lactation suggests a role in postnatal development of the mammary
gland
JOURNAL Mol. Cell. Biol. 12, 2418-2423 (1992)
FEATRES 92236617

JOURNAL

92236617
MEDLINE
AUTHORS Gavin,B.J. and McMahon,A.P.
TITLE Differential regulation of the Wnt gene family during pregnancy and
lactation suggests a role in postnatal development of the mammary
gland
JOURNAL Mol. Cell. Biol. 12, 2418-2423 (1992)
FEATRES 92236617

JOURNAL

92236617
MEDLINE
AUTHORS Gavin,B.J. and McMahon,A.P.
TITLE Differential regulation of the Wnt gene family during pregnancy and
lactation suggests a role in postnatal development of the mammary
gland
JOURNAL Mol. Cell. Biol. 12, 2418-2423 (1992)
FEATRES 92236617

JOURNAL

92236617
MEDLINE
AUTHORS Gavin,B.J. and McMahon,A.P.
TITLE Differential regulation of the Wnt gene family during pregnancy and
lactation suggests a role in postnatal development of the mammary
gland
JOURNAL Mol. Cell. Biol. 12, 2418-2423 (1992)
FEATRES 92236617

JOURNAL

92236617
MEDLINE
AUTHORS Gavin,B.J. and McMahon,A.P.
TITLE Differential regulation of the Wnt gene family during pregnancy and
lactation suggests a role in postnatal development of the mammary
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JOURNAL Mol. Cell. Biol. 12, 2418-2423 (1992)
FEATRES 92236617

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MEDLINE
AUTHORS Gavin,B.J. and McMahon,A.P.
TITLE Differential regulation of the Wnt gene family during pregnancy and
lactation suggests a role in postnatal development of the mammary
gland
JOURNAL Mol. Cell. Biol. 12, 2418-2423 (1992)
FEATRES 92236617

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DEFINITION Xenopus laevis wnt7B (Xwnt7B) mRNA, complete cds.
ACCESSION AF026894
VERSION AF026894.1 GI:2583210
KEYWORDS
SOURCE
ORGANISM
AFRICAN clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae;
Xenopus.
1 (bases 1 to 1199)
Chang,C. and Hemmati-Brienvlou,A.
Neural patterning by Xenopus wnt7B gene
Unpublished
2 (bases 1 to 1199)
Chang,C. and Hemmati-Brienvlou,A.
Direct Submission
Submitted (25-SEP-1997) Molecular Embryology, The Rockefeller
University, 1230 York Avenue, New York, NY 10021, USA
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RESULT 9

LOCUS CHRM4P 1427 bp mRNA VRT 23-JUN-1999

DEFINITION Chicken mRNA for Wnt-4 protein, complete cds.

ACCESSION D31900

VERSION D31900.1 GI:505351

KEYWORDS Wnt gene family; Wnt-4 protein; cysteine-rich secretory protein; growth factor.

SOURCE Gallus gallus (library: lambda gt10) embryo cDNA to mRNA, clone Wnt-4.

ORGANISM Gallus gallus

REFERENCE 1 (sites)

Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

Yoshida, H., Ohuchi, H., Nohno, T., Fujiwara, A., Tanda, N., Kawakami, Y., and Noji, S.

Regional expression of the Wnt-4 gene in developing chick central nervous system in relationship to the diencephalic neuromere D2 and a dorsal domain of the spinal cord

Biochem. Biophys. Res. Commun. 203 (3), 1581-1588 (1994)

2 (bases 1 to 1427)

Tanda, N., Kawakami, Y., Saito, T., Noji, S., and Nohno, T.

Cloning and characterization of Wnt-4 and Wnt-11 cDNAs from chick embryo

DNA Seq. 5 (5), 277-281 (1995)

96063018

3 (bases 1 to 1427)

Nohno, T.

Direct Submission

Submitted (20-JUN-1994) to the DDBJ/EMBL/GenBank databases. Tsutomu Nohno, Kawasaki Medical School, Department of Pharmacology; 577 Matsushima, Kurashiki, Okayama 701-01, Japan

(Tel:0864621111(ex.3637), Fax:0864621199)

Submitted (20-Jun-1994) to DDBJ by:

COMMENT

Journal

Medline

Reference

Authors

Title

Journal

Features

Source

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BASE COUNT 296 a 438 c 453 g 240 t

ORIGIN

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Qy 430 TTCCCAACCGCGCTGGAACGCTCCACGCTGACACCTCTGCTGTTGGCAAGTG 489

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SOURCE Norway rat.
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Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Rattus.
AUTHORS Lacher, M.D., Walthers, P.R., Lareu, R., Dharmarajan, A.M. and
Filiis, R.R.
TITLE Rat Wnt-4 mRNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1213)
AUTHORS Lacher, M.D., Walthers, P.R., Lareu, R., Dharmarajan, A.M. and
Filiis, R.R.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) Department of Clinical Research, University
of Berne, Telfenaustrasse 120, Berne 3004, Switzerland
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RESULT 12
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DEFINITION Mouse Wnt-4 mRNA, complete cds.
VERSION M89797
KEYWORDS Wnt-1 related protein; Wnt-4 protein; Int-1 related protein.
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1101)
AUTHORS Gavin, B.J., McMahon, J.A. and McMahon, A.P.
TITLE Expression of multiple novel Wnt-1/Int-1-related genes during fetal
and adult mouse development
JOURNAL Genes Dev. 4, 2319-2332 (1990)
MEDLINE 9112634
REFERENCE 2 (bases 1 to 1101)
AUTHORS Gavin, B.J. and McMahon, A.P.
TITLE Differential regulation of the Wnt gene family during pregnancy and
lactation suggests a role in postnatal development of the mammary
gland
JOURNAL Mol. Cell. Biol. 12, 2418-2423 (1992)
MEDLINE 92236617
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Db 437 GAGAACTGGAGAAGTGTGGCTGTGACCCGGACAGTGCAGCGGGTCAAGCCAC-----AGG 490
Qy 437 gctggaagtgggtgctgctgctgcccgaatccgctgagcatcggtctgcgcaagctc 496
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Qy 497 ttgtgagtcgccggagatcaagcagaatgc-----ccggaactctcatgaacttgc 547
Db 551 TTGTGGAGCTCCGGGAGAGAGACAAAGGGGCTCTCCACCGCGGCACTCATGAATCTTC 610
Qy 548 acaacaacagagcagagccgaagatccctgagagagaacacatgaagcttgaaatgac 607
Db 611 ACAACAAGAGCTGCGAGAGAGGCCATCTTGACACACATGGGGGGAGTGCACAGTGTG 670
Qy 608 acggcgctgcaagctcgctgacccaagaagctgctggaaccaactgccaagtttcgg 667
Db 671 ACGGGGTGTCGGGCTCTCCGAGAGTAAAGACGTGCTGGGCTCTGACCGCCCTTCGGC 730
Qy 668 agctggagctagcttcaaggaacaagtacagagccgttcaagctgagagccttgagct 727
Db 731 AGGTGGCCACCCGCTAAAGAGAGATTGACGGGTGCCAGAGGTGGGACACAGACGG 790
Qy 788 ccagccgcaacaagcggccacactctcctgtaagatcaagaagcgaactgtgtaacgcaagc 787
Db 791 TAGGTCCTCCCGGGGGGCTGCTCGGAATGACAC-----GTTCAGGCCAC 838
Qy 788 ccatggaacagagcctgtgttcatcatcgaaagctgcccaactactcgagagagcccg 847
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Db 899 GCAGTGGCGGTGCTAGGACGAGAGGGGCGCAGCTGCACAAACATCTTAACCATTTGACG 958
Qy 908 gctgtgacctaatgtgtgtgtggcggtggtctacaacaccacagtaagcccggtgtgc 967
Db 959 GCTGGACCTACTGCTGCTGTGGCGCGGCTTCACACAGCCCAAGTGGAGCTGGCCGAGC 1018
Qy 968 agtgaactgtgaagtccacgtgtgtctatgtcaagtgaacacagctgcaagcgca 1027
Db 1019 GCTGGCTGCAAGGTTCCAGTGTGCTCTTGTCAAGTGCAGGCAATGCCAGCGCTTCG 1078
Qy 1028 cgaagatgtacagctgtcaagtga 1050
Db 1079 TGGAGATGACACAGTGGCGGTGA 1101

RESULT 13
DMDMNT2MR 1252 bp mRNA INV 09-AUG-1996
LOCUS D melanogaster Dmnt-2 mRNA.
DEFINITION X64735
ACCESSION X64735.1 GI:7904
VERSION Dmnt-2 gene; Wnt/wingless gene.
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
Drosophilidae; Drosophila.
REFERENCE Russell, J., Gemmisen, A. and Nusse, R.
TITLE Isolation and expression of two novel Wnt/wingless gene homologues
in Drosophila
JOURNAL Development 115 (2), 475-485 (1992)
MEDLINE 93048811
REFERENCE Nusse, R.
TITLE Direct Submission
AUTHORS Submitted (02-MAR-1992) R. Nusse, Howard Hughes Medical Inst and
JOURNAL Dept of Developmental Biology, Stanford University, Stanford CA
94305, USA
FEATURES
source
location/Qualifiers
1..1252
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/db_xref="taxon:7227"
/dev_stage="embryo"
/map="45E on polytene chromosome"
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/allele="Wnt oncogene analog 2"
/db_xref="FlyBase:FBgn0004360"
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/feature="Wnt2"
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/db_xref="GI:7905"
/db_xref="FLYBASE:FBgn0004360"
/translation="MKIKHKLITVIMETRIIVSSFTSAMICGRIPGTCGRMNC
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ASGAAARVPAACARGNISTCGDVHRKATPTGGTPTDEPWKGGCSADVDFGRAR
LVDDRRLMKYOKAKTVQAVYKGRGLVLSRKHAAGTARAKQKVLDMPKMKELIYEA
SPNYCERSIOTGSGTSGRTGRTGTHGPGSCDILCGGRHNTHIRITQRCRQFRMC
CEVRCDECDSEYEPFCK"
BASE COUNT 309 a 349 c 365 g 227 t 2 others
ORIGIN
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QY 827 actactcgagagagaccggtgaccgcaagltgaggaccacagggccgctgcaaca 886
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Db 890 ACTTTGTGAGCCCAACCCAGAGAGGGCTCCTTGTATCCAGGGACCGACTTGCAATG 949
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QY 887 agacggtcccccagggccagggctgtgacctcaatgtctgtggcggtgctacaacacc 946
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 950 TCACCTCCACGGGATGATGCTGCGATCTGTCTGTGCGGGGCCCAACACGA 1009
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 947 accagtaagcccggtgtgagtgcaactgttaagtccactgtgtgtctatgtcaagt 1006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1010 GGACGGAGAAACGGAAGAGAAATGCCATTGCGTCTTCACCTGGTGTCTATGTACAGCT 1069
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1007 gcaacacgtgcaagcagcagcagcagagatgtacacgtgcaagt 1048
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1070 GCCAAGAGGTGTATCGCATCTACGATGTGCACACCTGCAAGT 1111
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rch completed: April 3, 2000, 04:12:53
time: 3036 sec

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WINGLESS (TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
on: Thu Mar 30 12:42:31 2000; Maspar time 89.67 Seconds
269,854 Million cell updates/sec

Tabular output not generated.

Title: >US-09-459-774-2
Description: (1-349) from US09459774.pep
Perfect Score: 2660
Sequence: 1 MNRKARRCLGHLFSLGMY.....NCQYKNCNTSEKTEKTC 349

Scoring table:
PAM 150
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database:

sptrembl12
1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_plant 10:sp_protist 11:sp_protein 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 46.372; Variance 68.126; scale 0.681

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2643	99.4	349	4	O9Y560	WNT7A PROTEIN.	0.00e+00
2	2387	89.7	348	13	O13265	WNT-7A.	0.00e+00
3	2312	83.2	349	13	O42258	WNT7B.	0.00e+00
4	1844	69.3	347	5	O61700	AMPHIANT7B.	0.00e+00
5	1097	41.2	385	13	O916X6	WNT-5A.	4.33e-265
6	1086	40.8	331	5	O96867	CELL SIGNALING MOLECUL	5.69e-262
7	1040	39.1	361	4	O9Y5C0	WNT16 PROTEIN.	6.02e-249
8	1010	38.0	370	13	P79752	WNT1.	1.82e-240
9	980	36.8	252	5	P91951	WNT-4 PROTEIN (FRAGMEN	5.35e-232
10	948	35.6	377	5	O61699	AMPHIANT1.	5.80e-223
11	885	33.3	354	13	O73864	WNT11 PROTEIN.	2.89e-205
12	875	32.9	350	11	O9WUD6	WNT8B PROTEIN PRECURSOR	1.85e-202
13	822	30.9	398	5	O23224	W08B2.1 PROTEIN.	1.28e-187
14	793	29.8	390	13	P79753	WNT10B.	1.59e-179
15	734	27.6	389	13	P79856	WNT-10A.	4.16e-163
16	680	25.6	121	13	O42119	WNT 7B (FRAGMENT).	3.72e-148
17	679	25.5	362	5	O16146	WNT-2.	7.03e-148
18	634	23.8	250	5	O26771	WINGLESS (FRAGMENT).	7.62e-145
19	634	23.8	381	5	O10459	HYPOTHETICAL 42.3 KD P	1.74e-135
20	558	21.0	178	5	O9Y0W0	MG MRNA, PARTIAL CDS (1.04e-114

21	534	20.1	123	5	O27070	WINGLESS/WNT HOMOLOGUE	3.39e-108
22	432	16.2	91	13	O31121	WNT-5B (FRAGMENT).	7.56e-81
23	423	15.9	348	5	O27886	WNT PROTEIN.	1.82e-78
24	411	15.5	120	5	O17149	WNT-A PROTEIN (FRAGMEN	2.68e-75
25	395	14.8	118	13	O42116	WNT 4 (FRAGMENT).	4.29e-71
26	378	14.2	127	13	O91229	WNT-1 PROTEIN (FRAGMEN	1.19e-66
27	364	13.7	128	5	O76780	HYPOTHETICAL 14.4 KD P	5.20e-63
28	361	13.6	114	13	O42117	WNT 5A (FRAGMENT).	3.12e-62
29	357	13.4	118	5	O17150	WNT-B PROTEIN (FRAGMEN	3.38e-61
30	345	13.0	111	5	O96868	CELL SIGNALING MOLECUL	4.21e-58
31	326	12.3	111	5	O96869	CELL SIGNALING MOLECUL	3.11e-53
32	325	12.2	141	5	O25533	WINGLESS PROTEIN (FRAG	5.60e-53
33	317	11.9	115	13	O42118	WNT 6 (FRAGMENT).	6.08e-51
34	305	11.5	84	5	O46291	WINGLESS (FRAGMENT).	6.63e-48
35	304	11.4	84	5	O46281	WINGLESS (FRAGMENT).	1.19e-47
36	302	11.4	84	5	O46301	WINGLESS (FRAGMENT).	3.79e-47
37	302	11.4	84	5	O46287	WINGLESS (FRAGMENT).	3.79e-47
38	302	11.4	84	5	O46297	WINGLESS (FRAGMENT).	3.79e-47
39	302	11.4	84	5	O46277	WINGLESS (FRAGMENT).	3.79e-47
40	302	11.4	84	5	O46275	WINGLESS (FRAGMENT).	3.79e-47
41	301	11.3	126	13	O98994	WNT10B PROTEIN (FRAGME	6.76e-47
42	299	11.2	84	5	O46303	WINGLESS (FRAGMENT).	2.15e-46
43	298	11.2	130	13	O98903	WNT10B PROTEIN (FRAGME	3.84e-46
44	296	11.1	84	5	O46293	WINGLESS (FRAGMENT).	1.22e-45
45	284	10.7	86	5	O26243	CELL-CELL COMMUNICATIO	1.23e-42

ALIGNMENTS

RESULT 1
ID O9Y560 PRELIMINARY; PRT; 349 AA.

DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE WNT7A PROTEIN.
GN WNT7A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eukaryota; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97049094.
RA IREKANA S., KUMANO Y., OKUI K., FUJIMURA T., TAKAHASHI E.,
RA NAKAMURA Y.;
RT "Isolation, characterization and chromosomal assignment of the human
RT WNT7A gene.";
RL Cytogenet. Cell Genet. 74:149-152(1996).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
DR EMBL; D83175; BAA82509.1; .
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein.
SQ SEQUENCE 349 AA; 39057 MW; 9C18E1B2 CRC32;

Query Match 99.4%; Score 2643; DB 4; Length 349;
Best Local Similarity 99.1%; Pred. No. 0.00e+00;
Matches 346; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db	1	MNRKARRCLGHLFSLGMYVIRIGGSSVVALGASIIICNKPGLAPRQRAICQSPRAII	60
Qy	1	MNRKARRCLGHLFSLGMYVIRIGGSSVVALGASIIICNKPGLAPRQRAICQSPRAII	60
Db	61	VIGGSSQMGIDECOPFQPNRGNWNCALGERTVFSKELKVSREAAFYAIIAAGVAHAIT	120
Qy	61	VIGGSSQMGIDECOPFQPNRGNWNCALGERTVFSKELKVSREAAFYAIIAAGVAHAIT	120
Db	121	AACQGNLSDCGCGKKEKGGVYHREDEGKMKWGCSADIRYIGISFAVYFADARIKQNTATIM	180

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QY 121 AACTGNSIDCGDCEKQGYHDEGWMKGGCSADIRYIGIKAFVADAREIKONARTLM 180
DB 181 NLHNEAGRKILIEENMKLECKCHGVSGSCTTKTCTTLPQFRELGYVLKDKNEAVHVP 240
QY 181 NLHNEAGRKILIEENMKLECKCHGVSGSCTTKTCTTLPQFRELGYVLKDKNEAVHVP 240
DB 241 VRASNNKRPFLKIKKPLSYRRKPMDTLVYIEKSPNYCEDPVTSVGTQGRACKNTAPQ 300
QY 241 VRASNNKRPFLKIKKPLSYRRKPMDTLVYIEKSPNYCEDPVTSVGTQGRACKNTAPQ 300
DB 301 ASGCDLMCCGGRGYNTHOYARVWCNCKFHMCCYVCNCTCSETEMYTCK 349
QY 301 ASGCDLMCCGGRGYNTHOYARVWCNCKFHMCCYVCNCTCSETEMYTCK 349

RESULT 2
ID 013266 PRELIMINARY: PRT: 348 AA.
AC 013266:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
PT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
QY 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
WNT-7A.
Pleurodeles waltl (Iberian ribbed newt).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Caudata; Salamandroides; Salamandridae; Pleurodeles.
RN [1]
RP SEQUENCE FROM N.A.
RA CAUBIT X., NICOLAS S., LE PARCO Y.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
CC DR EMBL; U80581; AAB58494.1; -.
CC DR PROSITE; PS00246; WNT1; 1.
CC DR PFM; PF00110; wnt; 1.
CC KW Developmental protein; Glycoprotein.
CC SEQUENCE 348 AA; 39039 MW; 5F951309 CRC32;

Query Match 89.7%; Score 2387; DB 13; Length 348;
Best Local Similarity 87.4%; Pred. No. 0.00e+00;
Matches 305; Conservative 30; Mismatches 13; Indels 1; Gaps 1;

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ID 042258 PRELIMINARY: PRT: 349 AA.
AC 042258:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
PT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
QY 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
WNT7B.
GN XWNT7B.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANG C., HEMMATI-BRIVANLOU A.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
CC DR EMBL; AF026894; AAB82725.1; -.
CC DR PROSITE; PS00246; WNT1; 1.
CC DR PFM; PF00110; wnt; 1.
CC KW Developmental protein; Glycoprotein.
CC SEQUENCE 349 AA; 39740 MW; B665D4B5 CRC32;

Query Match 83.2%; Score 2212; DB 13; Length 349;
Best Local Similarity 78.2%; Pred. No. 0.00e+00;
Matches 273; Conservative 50; Mismatches 26; Indels 0; Gaps 0;

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MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
SIMILARITY).

-1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXTRACELLULAR MATRIX.

-1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.

EMBL: AF061975; AAC80433.1; -

DR PROSITE: PS00246; WNT1.1.

DR PFAM: PF00110; wnt.1.

KW Developmental protein; Glycoprotein.

SEQUENCE 347 AA; 39425 MW; CF2DA66 CRC32;

Query Match 69.3%; Score 1844; DB 5; Length 347;
Best Local Similarity 65.1%; Pred. No. 0.00e+00;
Matches 224; Conservative 69; Mismatches 46; Indels 5; Gaps 5;

8 RYLGA-V-LCVA-1-LQGLSLTVVALGANIICNRIPLGLVPRRAICQTRPDLIVAGSGA 64
7 RCLGLHLFLSLGMVYLRIIGFSSVALGASIIICNRIPLGLAPRAICQSRPAIIYIGSGS 66
65 QRGIDCEKTYQRRHSMNCTGNDNVPFRELIGSKFAFYTAISSALVHAIVTACSG 124
67 QMGDECFQFQRRGKMNCSALGERVFGKELKVSREAFYAITAGVHAHITACG 126
125 NISDGGCORTKEDLN-DEGMWGGCSADVYKGLRCKKFPDAREVQNNARMLNHNNE 183
127 NLSDCGCKEKQGTGHRDEGMWGGCSADIRIGFAKVPDARFQNKARMLNHNNE 186
184 AGRVVDQHTLECKCHGVSSTCTKTCMTLTPREFVGNILKEKYHDAQVLEAVRAR 243
187 AGRILLENMMLCKECHGVSGCTKTCMTLTPREFVGNILKEKYHDAQVLEAVRAR 245
244 TRPPTFLKASRPFKREISLYLGRSPVNCEDATGSLTGRCNRTSPYQDCD 303
246 NKRPTEFLKIKRPLSYRPMDDLYIEKSPNCEDEPTGSGYQGRACNRTAPQASGD 305
304 LMCGRGYNTHOYFVTCNCKFHMCCYVKNQCSERTETCK 347
306 LMCGRGYNTHOYFVTCNCKFHMCCYVKNQCSERTETCK 349

RESULT 5 PRELIMINARY; PRT: 385 AA.

ID 09YX6;
AC 09YX6;
DT 01-MAY-1999 (Tremblrel. 10, Created)
01-MAY-1999 (Tremblrel. 10, Last sequence update)
01-NOV-1999 (Tremblrel. 12, Last annotation update)
WNT-5A.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-EMBRYO.
RX MEDLINE: 99372672.
RA KAKAKAMI Y., WADA N., NISHIMATSU S., ISHIKAWA T., NOJI S., NOHNO T.;
RT "Involvement of wnt-5a in chondrogenic pattern formation in the chick
limb bud.";
RL Dev. Growth Differ. 41:29-40(1999).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
SIMILARITY).

-1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXTRACELLULAR MATRIX.

-1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.

EMBL: AB060614; BAAT5242.1; -

DR PROSITE: PS00246; WNT1.1.

KW Developmental protein; Glycoprotein.

SEQUENCE 385 AA; 43005 MW; 1C8EA6D9 CRC32;

Query Match 41.2%; Score 1097; DB 13; Length 385;
Best Local Similarity 47.3%; Pred. No. 4.33e-265;

Matches 157; Conservative 67; Mismatches 90; Indels 18; Gaps 9;

63 SEVYITGAQPLCSLAGISGCKLQYODHMFQIGAGTKECOYFRHRMNCST 122
27 SSVVALGASIIICNRIPLGLAPRAICQSRPAIIYIGSGOMGDECFQFRRGKMNCSA 86
123 VDNNSVFERVWQISREAFYTAISAGVNAVRACGEGLSSCGSRARPPDLPLD 181
87 LGERTVFGKELKVSREAFYTAISAGVNAVRACGEGLSSCGSRARPPDLPLD 145
182 -WLVGGCSDNIETGYRFAKEFVADARERERYQGRSYESARIMMLNHNNEAGRTVYNLAD 240
146 GKNKGGCSADIRIGFAKVPDARE---I--K---QARILMLNHNNEAGRTVYNLAD 197
241 VACCHGVSGCSLCTKWLQADFRKYGDALEKERYDSAAAK-L-NSRCK---L-VQNN 293
198 LECKCHGVSGCTKTCMTLTPREFVGNILKEKYHDAQVLEAVRAR 257
294 SRFNAPTHDLYIDPSDYGMRNBSGSLGTGRLCKTSEGMDGCLMCCGSGYDQFK 353
354 TVQERCHCKRPFHMCCYVCKLCTEIVDQVCK 385
318 YARWQCNCKRPFHMCCYVCKNCTSERTEMTYCK 349

RESULT 6 PRELIMINARY; PRT: 331 AA.

ID 096867;
AC 096867;
DT 01-MAY-1999 (Tremblrel. 10, Created)
01-MAY-1999 (Tremblrel. 10, Last sequence update)
01-NOV-1999 (Tremblrel. 12, Last annotation update)
CELL SIGNALING MOLECULE WNT-5 (FRAGMENT).
GN SPNWT-5.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidae;
OC Echinozoa; Echinodermata; Echinoidae; Strongylocentrotidae;
OC Strongylocentrotus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98320638.
RA FERKOWITZ M.J., STANDER M.C., RAFF R.A.;
RT "Phylogenetic relationships and developmental expression of three sea
urchin Wnt genes.";
RL Mol. Biol. Evol. 15:809-819(1998).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
SIMILARITY).

-1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXTRACELLULAR MATRIX.

-1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.

EMBL: U58982; AAC69436.1; -

DR PROSITE: PS00246; WNT1.1.

KW Developmental protein; Glycoprotein.

FT NON_TER
SEQUENCE 331 AA; 36989 MW; A94F2700 CRC32;

Query Match 40.8%; Score 1086; DB 5; Length 331;
Best Local Similarity 50.2%; Pred. No. 5.69e-262;
Matches 164; Conservative 53; Mismatches 92; Indels 18; Gaps 10;

14 LGTGPLCELSLSPGQKLCQLYODHMAIPGEAKSIDSCQNFQTRRNKSTVDSNN 73
32 LGASTICKIKIGLAPRAICQSRPAIIYIGSGOMGDECFQFRRGKMNCSALGERT 91
74 VFGKYLSSRREAFYTAISAGVNAVRACGEGLSSCGGKSPRPDIPD-L-VWYG 131
92 VFGKELKVSREAFYTAISAGVNAVRACGEGLSSCGGKSPRPDIPD-L-VWYG 150
132 GCGNIDYGFARFVADAREMTNPGQSFAYRBMKMLNHNNEAGRTVYNLAD 191

OY 151 GCSADIRYIGIFAKVFDAREIKONA-R--T--L-NMHNHNEAGRKILLENMKLECKC 202
 DB 192 HGVSGSCSLKTCWLOLSPENRYGTLKDYDGTATY--RV--NKKGR-L-VNSDARFK 244
 OY 203 HGVSGSCSLKTCWTLTPORRELYVAKDKYNEVHEPRASRNKRPFLTKIKPLSTYK 262
 DB 245 PRRDLYVLPSPDYCLPDIGTSLGTTGREGCNISMTGDTLMCCGRGNSFTKEYE 304
 OY 263 PMDTDLVYIEKSPNCEEDPYTGVGTGRACNKTAPQASGCDLMCCGRGNTHQYARVW 322
 DB 305 RCKCFKCCYVCKCRKCRITLVYHNC 331
 OY 323 QCNCFHMCYVCKNCTSERTEYTC 349
 RESULT 7 PRELIMINARY: PRT: 361 AA.
 AC 09Y5C0:
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DT WNT16 PROTEIN.
 WNT16.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RC TISSUE=PLACENTA;
 RA BARNES M.R., KELSELL D.P., FEAR M.W.;
 RT "Cloning and characterization of human Wnt16, a novel member of the
 RT Wnt gene family."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF155584; AAD38052.1; -
 SQ SEQUENCE 361 AA: 40558 MW: D59A8ED6 CRC32:

Query Match 39.1%; Score 1040; DB 4; Length 361;
 Best Local Similarity 44.6%; Pred. No. 6, 02e-249;
 Matches 145; Conservative 76; Mismatches 85; Indels 19; Gaps 11;

DB 43 CANLP-LNSROELCKRKRYLLPSIREGARKLIGECRSOFREBRNMTTAATAPMCA 101
 OY 38 CNKIGELAPROAICOSRDAITVIGESQMGIDECQFOFRNGRNC-----SA-LGE 89
 DB 102 SPLFGYELSGTETAFIYAVMAAGLVHSVTRSCSAGNTECSQDTTLQNGSASGWH 161
 OY 90 RYVFGKELKVGSRFAFTAITAAGVAHAITACTGNTSDGCDKEKQYHRDEGMW 149
 DB 163 GGCSDVOYGMFSSKFLDFPIGNTGKENKYLAMNHNHNEAGROAVAKLMSVDCRCHG 221
 OY 150 GGCSDIRYIGIFAKVFD-AR-EIK-QNARTL--MNLHNNEAGRKILLENMKLECKCHG 204
 DB 222 VSGSCAVKTCWMTMSFEIIGHLDKYENSIOISD-KIKRKKRR-EXDQKRIPIHK-- 277
 OY 205 VSGSCITTKCMTTLTPORRELYVAKDKYNEVHEPRASRNKRPFLTKIKPLSTYK 264
 DB 278 D-DLYVNSPKNYCYEDKLGIGTGTGREGCNISMTGDTLMCCGRGNTHQYARVW 336
 OY 265 DTDLYVIEKSPNCEEDPYTGVGTGRACNKTAPQASGCDLMCCGRGNTHQYARVW 324
 DB 337 ECKFTWCCYVCKCRKCRITLVYHNC 361
 OY 325 NCKCFHMCYVCKNCTSERTEYTC 349
 RESULT 8 PRELIMINARY: PRT: 370 AA.
 AC P79752:
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE WNT1.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphia;
 OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA GELLNER K., BRENNER S.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
 CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
 CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
 CC EXTRACELLULAR MATRIX.
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
 DR EMBL: AF056116; AAC34388.1; -
 DR PROSITE: PS00246; WNT1. 1.
 DR PIRAM: PF00110; wnt. 1.
 DR Developmental protein; Glycoprotein.
 SQ SEQUENCE 370 AA: 41050 MW: 1412B124 CRC32:

Query Match 38.0%; Score 1010; DB 13; Length 370;
 Best Local Similarity 43.5%; Pred. No. 1, 82e-240;
 Matches 135; Conservative 67; Mismatches 100; Indels 8; Gaps 6;

DB 63 LSRRORLIRONPGILHAIAAGLHAIAKECKWOFNRNRNCPTHSPAVFGKIYNGCRE 122
 OY 44 LAPRRAICQSRPDALIIYIGESQMGIDECQFOFRNGRNCALGERIVFELKLVGSR 103
 DB 123 TAFVFAISAGYTAHAVASCEGAIEFCTCYRRGP--GGPDHMGCCSNVEGRMFS 180
 OY 104 AAFYFAIITAGVAHAITACTGNTSDGCDKEKQYHRDEGMWGCSDIRYIGIFA 163
 DB 161 REFVSSRGRLRLTLNHNHNEAGRMVTSSEMBOECKCHGMSGCVRYTCWMLPSRM 240
 OY 164 KVFVDAIREIKOARTLNMHNHNEAGRKILLENMKLECKCHGVSSCTTKTCWTLTPORE 223
 DB 241 VDFPLKDFEDGASRYVYANKSNSRASHRAHPRIEENP-AHKPPSSMDLYFEPKSPNFC 299
 OY 224 LGYVLKDYNEVHE-PRAS-R-NKR--PFLKIKRPLRYRPMDDLYVIEKSPNYC 278
 DB 300 SYSKGTGLTSGRACNSTSPGLDCELLCCGRGKRTESMTBCHCTFRMCHVSCLN 359
 OY 279 EEDPYTGVGTGRACNKTAPQASGCDLMCCGRGNTHQYARVWQCNCKCFHMCYVCKNT 338
 DB 360 CSTRTTLHQC 369
 OY 339 CSERTEYTC 348
 RESULT 9 PRELIMINARY: PRT: 252 AA.
 AC P91951:
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE WNT-4 PROTEIN (FRAGMENT).
 GN HEWNT-4.
 OS Helicodactylis erythrogramma (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
 OC Euechinozoa; Echinozoa; Echinozoa; Echinomelittidae; Helicodactyls.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA FERROWICZ M.J., STANDER M.C., RAFF R.A.;
 RL J. Mol. Evol. 0.0-0.00.
 CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
 CC MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
 CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
 CC EXTRACELLULAR MATRIX.
 CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
 DR EMBL: U88626; AAC69242.1; -
 DR PROSITE: PS00246; WNT1. 1.

PFAM: PF00110; wnt: 1.
DR Developmental protein: Glycoprotein.

FT NON TER 1
SQ SEQUENCE 252 AA; 27844 MM; 889959C0 CRC32;

Query Match 36.8%; Score 980; DB 5; Length 252;
Best Local Similarity 50.2%; Pred. No. 5,356-232;

Matches 130; Conservative 50; Mismatches 69; Indels 10; Gaps 9;

Db 1 GHVLDNGREAFVNAISAAGVANAATVTCSSGGELEKCCDR-IVGG-NSAGETVWAGCS 58

94 GKELVSGREAFVNAISAGVANAATVTCSSGGELEKCCDR-IVGG-NSAGETVWAGCS 153

Db 59 DNVAAGVQSFQTVAMERKTRATLERLMHNHNEAGRTLEEMRECKCHGSSCE 118

154 ADIRYIGFAVYDAREIK-QNA-RTLMNHNHNEAGRTLEEMRECKCHGSSCT 210

Db 119 MKTCMSKPTREGDIGHVLEKEFGDTEVSLKIG-S-ROQ-L-VPRIADFPHTSSDLV 174

211 TKTCMTLTPQRELGYLKKDYNEAVHEPVASRNRKPTLKKPLSTYRKPMOTDLV 270

Db 175 LVSPDPCEDD-LVSGDTHGRCKTSKAIIDCELMCCGRTHTIEVIERSCRTFW 233

271 IEKSPNCEEDPVYGVTOGRACNKTAPQASGCDLMCCGRGYTHOYARVWQCCKEFHW 330

Db 234 CCYVCRNCHRTVEVHTCK 252

331 CCYVCRNCHRTVEVHTCK 349

RESULT 10 PRELIMINARY; PRT: 377 AA.

ID 061699; AC 061699;

DT 01-AUG-1998 (Tremblrel. 07, Created)

DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)

DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)

DE AMPHIMNT1.

GN WNT1.

OS Branchiostoma floridae (Florida lancelet) (Amphioxus).

OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;

CC Branchiostoma.

RN [1]

RP SEQUENCE FROM N.A.

RA SCHUBERT M., HOLLAND L.Z., JACOBS D.K., HOLLAND N.D.;

RT "Isolation of Amphimnt1, Amphimnt4, Amphimnt7a and Amphimnt7b from the

Cephalochordate Amphioxus and Evolution within the Wnt Gene Family of

Invertebrates and Vertebrates."

Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING

MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF

TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY

SIMILARITY).

CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE

EXTRACELLULAR MATRIX.

CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.

DR EMBL: AF061974; AAC80432.1; .

DR PROSITE: PS00246; WNT1.1.

DR PFAM: PF00110; wnt: 1.

KW Developmental protein: Glycoprotein.

SQ SEQUENCE 377 AA; 42401 MM; B265CC49 CRC32;

Query Match 35.6%; Score 948; DB 5; Length 377;
Best Local Similarity 42.3%; Pred. No. 5,606-223;

Matches 18; Conservative 64; Mismatches 11; Indels 13; Gaps 11;

Db 54 GSTIMLDKRPPLNKKORLVRNNGDAGEHRRPMLAIKECHHGFQKMNCPVNTSD 113

33 GASITCN-KINGLAPRGALICOSRDALIVGEGSQ-GDECCQGFNGRNNGCA-LGE 89

Db 114 HNSVFGNILLGCTQTAFITAVMSAAVAHEVGRNCAEGTETGSCDYRSKGP--AGSDW 171

90 R-IVFGKELVSGREAFVNAISAGVANAATVTCSSGGELEKCCDR-IVGG-NSAGETVWAGCS 147

Db 172 EMGGSNDVVEFGKQAFQVADAGEKTKDSVRYLVNHNHNEAGRTLEEMRECKCHGMS 231

148 KWGGSADIRYIGFAVYDAREIK-QNA-RTLMNHNHNEAGRTLEEMRECKCHGMS 206

Db 232 GSCTLKTCMRLPNFRDVGSLKEKFDGASKVAPEDIGNNGSRAKYTLGPKNSRHKP 291

207 GSCTTKCTMTLTPQRELGYLKKDYNEAVHEPVASRNRKPTLKKPLSTYRKPMOTDLV 263

Db 292 TDNDLVYHERSPNCRNRPGRFEGTGRRECNTVSRKIDGCDLLCCGRTHTIEVIER 351

264 MDTLVLYEKSPPNCEEDPVYGVTOGRACNKTAPQASGCDLMCCGRGYTHO-YARVW 322

Db 352 -CNCTFOMCCOVKCECVRTHTIC 376

323 QCNKFTWCYKCNCTCSRTMTTC 348

RESULT 11 PRELIMINARY; PRT: 354 AA.

ID 073864; AC 073864;

DT 01-AUG-1998 (Tremblrel. 07, Created)

DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)

DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)

DE WNT11 PROTEIN.

GN WNT11 OR WNT11.

OS Brachydonto rerio (zebrafish) (zebra dario).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;

Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Cyprinidae; Rasbora; Danio.

RN [1]

RP SEQUENCE FROM N.A.

RA MAKITA R., MIZONO T., KUROIWA A., KOSHIDA S., TAKEDA H.;

RT "Zebrafish wnt11: pattern and regulation of the expression by the yolk

cell and No tail activity."

Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING

MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF

TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY

SIMILARITY).

CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE

EXTRACELLULAR MATRIX.

CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.

DR EMBL: AF067429; AAC17922.1; .

DR HSSP: P81458; IYIP.

DR ZFIN: ZDB-GENE-980526-249; wnt11r.

DR PROSITE: PS00246; WNT1.1.

DR PFAM: PF00110; wnt: 1.

KW Developmental protein: Glycoprotein.

SQ SEQUENCE 354 AA; 39150 MM; 52888BFA CRC32;

Query Match 33.3%; Score 885; DB 13; Length 354;
Best Local Similarity 36.7%; Pred. No. 2,896-205;

Matches 127; Conservative 74; Mismatches 134; Indels 11; Gaps 8;

Db 15 LSVIYPCIGISWLGITNGSSVGNQTHCKLGLVDPDOQLCKRLNLMHSIVRAARL 74

9 LGHFLSLGAVYLRIGGSSVVALGASITCNKIKIGLAPRGALICOSRDALIVGEGSQ 68

Db 75 TKSACTSFSMDRNWNSIESAPHTPDLAGCTREAFVNAISAGVANAATVTCSSGGELEKCCDR-IVGG-NSAGETVWAGCS 134

69 GLDECOFQFRGNWNCALGERTVFGKELVSGREAFVNAISAGVANAATVTCSSGGELEKCCDR-IVGG-NSAGETVWAGCS 128

Db 135 PSCSCA-AMPSE-QAAPDFWGGGCDMLRYGLMGSAFSDAPMRNRSGPDRFLMQLH 192

129 SDGCGDKRQGYRDEGKMGWGSADIRY-GIGFAKVFDA--REIKONART--LWMLH 183

Db 193 NNAAGROYLMSLEMKCKCHGVSSCSYKTKWKLQDSTISADLSKYLSATVTP-RO 251

184 NNEAGRTLEEMRECKCHGVSSCSYKTKWKLQDSTISADLSKYLSATVTP-RO 243

Db 252 IGTRO--L-VPREVEVPVENEIVLVSPDCTONAKGSLGTDTROCNKTAAGSSES 308

QY 244 SNNKPTFLIKIKKPLSYRPMPTDLVIYIKSPNYCEDPVTSGTQGRACKTAPQASG 303
DB 309 CGLMCCGGRYNATYEVLEVERCOCKYHMCYSCCTCKRTVERVRSK 354
QY 304 CGLMCCGGRYNATYEVLEVERCOCKYHMCYSCCTCKRTVERVRSK 349

RESULT 12
ID Q9WUD6 PRELIMINARY; PRT: 350 AA.
AC Q9WUD6;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE WNT8B PROTEIN PRECURSOR.
GN WNT8B.
OS Mus musculus (Mouse).
OC Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
BC RICHARDSON M., REDMOND D., WATSON C., MASON J.O.;
RT "Mouse Wnt8b is expressed in the developing forebrain and maps to
chromosome 19.";
RL Mamm. Genome 0:0-0(1999).
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
CC EXTRACELLULAR MATRIX.
CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.
DR EMBL: AF130349; AAD31816.1; -.
DR PROSITE: PS00246; WNT1.1.
KM Developmental protein: glycoprotein.
SQ SEQUENCE 350 AA; 38576 MW; 89442A96 CRC32;

Query Match 32.9%; Score 875; DB 11; Length 350;
Best Local Similarity 42.4%; Pred. No. 1,85e-202;
Matches 125; Conservative 64; Mismatches 94; Indels 12; Gaps 8;

DB 42 VAAGASGIEECKYOFAMRNMCPERALDLSHG-GLRSANETAVVAISSAGWYITL 100
QY 62 IEBSQMGIDECOFQFRNRMNSALG-ERTYFGKELKGSREAPYAIAGVAHAAT 120
DB 101 RNCSLGDFNCGCDSDRNGOLG-GGGLMGSGSDNYGFEAISKOPVDALETGODARAA 159
QY 121 AACTGNTLSDCCGDKKQGYHDEBGMKGGCSADIRIGIFAKYVVDAREIKONARTLM 180
DB 160 NLHNNEAGRAVAKGTMKRTKCHGVSGSCTQTCWLDLPEFREYVAHLKRYAALVKDL 219
QY 181 NLHNNEAGRAVAKGTMKRTKCHGVSGSCTQTCWLDLPEFREYVAHLKRYAALVKDL 240
DB 220 LOGAGNSAAGRAALAD--TFRSISTRELYHLEDSPLYCKENTLGLTGEGRECLARGA 277
QY 241 VASASRKRPTFLKIKKPLSYRPMPTDLVIYIKSPNYCEDPVTSGTQGRACKTAPQASG 297
DB 278 LGRWERSRCRLCGDGLAVEERBATVSSCKNCFMCCAVCEOCRRRTVATFC 332
QY 298 -AP-QASGCDLMG--CGRGYNTHQYARVWQCNCKRFHMCYVACNTCSETEMTTC 348

RESULT 13
ID Q23224 PRELIMINARY; PRT: 398 AA.
AC Q23224;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE W0802.1 PROTEIN.
GN W0802.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditidae; Rhabditidae; Peloderiinae; Caenorhabditis.

RN (1)
RP SEQUENCE FROM N.A.
RA SWINBURNE J., AINSCOUGH R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIR M., JOHNSTON L.,
RA JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKIN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROUT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: 270271; CAA94237.1; -.
DR PFMW: PF00110; wnt.1.
SQ SEQUENCE 398 AA; 45843 MW; F54ACC1 CRC32;

Query Match 30.9%; Score 822; DB 5; Length 398;
Best Local Similarity 39.8%; Pred. No. 1.28e-187;
Matches 135; Conservative 79; Mismatches 96; Indels 29; Gaps 19;

DB 63 ICRRLDGLNPQNALCAENPSPFVARGVREAIKRECNKRFERNWSSDDEVETRHG 122
QY 37 ICKNIPGLAPQORATQSPRAIIVIGESQMGDECOFRNGWNCSA--LGE-R-- 90
DB 123 KFODILGTLSSANKAEFLNMAISVHSITKGCNGNTEGCDG--KPGMORYQAS 181
QY 91 T--VFGELEKYGSRFAFTYAIAGVAHAITACITGNSDCCGDKERKQ-Q-YHND- 144
DB 182 DPMNRDQFSWGGCSNDYPHGIRAKKFLDWMETAQDFKTNVAHLVRRHNFYGREIA 241
QY 145 E--GW-K--MGCSADIRYIGIFAKYVVDAREIKQ-N-ARTLMN--HNNENGRKILE 193
DB 242 QNIRQCRCHGVSGCEKRTKWLQMKSOVSDDLKKRYHFNAYVELEDYTR-KATRL 300
QY 194 ENMKLECKCHGVSGSCTKCTMTLLPQRELGYLKDYN--AAHVEVRSASRNKRPFL 252
DB 301 R-RKERTERKIPLRNGENAAVYHRSFYCEKMLTLAGILTSRECIHNSSESDLLCCG 359
QY 253 KIKKRLSYRK-PM-DTDLVIYIKSPNYCEDPVTSGTQGRACKTAPQASGCDLMCG 310
DB 360 RGYNTRLEIRQTCCKCFVWCCEYKCKTCEVAVHTCK 398
QY 311 RGYNTHQYARVWQCNCKRFHMCYVACNTCSETEMTTC 349

RESULT 14
ID P79753 PRELIMINARY; PRT: 390 AA.
AC P79753;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE WNT10B.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN (1)
RP SEQUENCE FROM N.A.
RA GELINER K., BRENNER S.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING
MOLECULE WHICH AFFECT THE DEVELOPMENT OF DISCRETE REGIONS OF
CC TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE

EXTRACELLULAR MATRIX.

CC -1- SIMILARITY: TO OTHER MEMBERS OF THE WNT FAMILY.

DR EMBL: AF056116; AAC34389.1; -

DR PROSITE: PS00246; WNT1.1.

DR PIRAM: PF00110; wnt.1.

KW Developmental protein; Glycoprotein.

SQ SEQUENCE 390 AA; 43656 MW; B432800B CRC32;

Query Match 29.8%; Score 793; DB 13; Length 390;

Best Local Similarity 40.3%; Pred. No. 1,59e-179; Mismatches 100; Indels 33; Gaps 19;

Matches 141; Conservative 76; Mismatches 100; Indels 33; Gaps 19;

Db 42 LTPNSVCLKLAGSKRQRMKVRSPDASALOGIOVAIHSCYOQLRQDQNNCSLEGLG 101

Y 32 LGASIIKIKIGLAPROALIQSRDAIIVIGESQMGDLDCQFQFRGNCSL-G-E 89

Db 102 KLPHNNTLNGFRESAFSLMLAAGVAHSAVSAACSMGKLGCCGCAKRRDDDKIRKL 161

Y 90 R-TVEGKELKVGSRBAATYAIAGVAHAITACTGCLDCCGD-K-----EK----- 137

Db 162 TOLQLOSLQKXDLDSMOETWEGSHDVRVGRDPRDLRSGSPRDIHBMKIHNNRV 221

Y 138 -Q-G-Q-YHRE--G---WKGCCSADIRYIGIPAKYVDAREIKQARTLMLHNEA 187

Db 222 GROIVTDMKRKCKCHTSGSCQFQTCWHSPEFRLVGLKEKELSAIIVSNQKNNGV 281

Y 188 GRKLEEMKLECKCHGVSCTTKTTLQFRELGYLKDKNVAVHEP-VRAS-R 245

Db 282 FNPIGSGVSGTGLNGRRSRSLVYFEKSPDFCEPILSVDSAGTQGRICKTSQS 341

Y 246 -NKR-PTFLKIKRP-LS--YRKPMOTDLYIEKSPNYCEEDPVTSVGTGACNKTAPO 300

Db 342 TDSGSLCCGGRHNLTKHSEKCRFHMCCYVCECRL-TEWYVYCK 390

Y 301 ASGCDLMCGGNTHTOYARWQCCKFHMCCYVCACTCSEKTE-MYTKC 349

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Db 219 DIHARMLHNNRVGROVLDNMGRKCKCHTSGSCQKTCQWYPERFVYNNLLKDRPHG 278

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